

1/13

1 ACAAGAATCT GCATTACACC ATGTACTTTT TCATCTGTAG CCTGGCTGTG
51 GCTGATATGC TGGTGAGCGT TTCCAATGGG TCAGAAACCA TTGTCAATCAC
101 CCTATTAAAC AGCACGGACA CGGACGCACA GAGTTTCACA GTGAATATTG
151 ATAATGTCAT TGAATCAGTG ATCTGTAGCT CCTTACTCGC CTCGAATTTGC
201 AGCCTGCTTT CGATTGCAGT GGACAGGTAT TTTACTATCT TTTATGCTCT
251 CCAGTACCAT AACATTATGA CAGTTAAGCG GGTGGAATC ATCATCAGTT
301 GTATCTGGC AGTCTGCACG GTGTCGGGTG TTTTGTTCAT CATTACTCA
351 GATAGCAGTG CTGTTATTAT CTGCCTCATA ACCGTGTTCT TCACCATGCT
401 GGCTCTCATG GCTTCTCTCT ATGTCCACAT GTTCCTCAIG GCCAGACTCC
451 ACATTAAGAG GATCGCCGTC CTCCCAGGCA CTGGCACCAT CCGCCAAGGT
501 GCCAACATGA AGGGGGCAAT TACCCTGACC ATCTTGATTG GGGTCTTTGT
551 GGTCTGCTGG GCCCCCTTCT TCCTCCACTT AATATTCTAT ATCTCCTGCC

Fig. 1

2/13

601 CCCAGAAATCC ATACTGTGTG TGCTTCATGT CTCACCTTTAA TTTGTATCTC
651 ATCCTGATCA TGTGTAATTC CATCATCXAT CCCCTGATTT ATGCACTCCG
701 GAGCCAAGAA CTGAGGAAA CCTTCAAAGA GATCATCTGT TGCTAT

Fig. 1A

Fig. 2B

5/13

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con-mc4r.seq 520 530 540 550 560 570
AGGGGCAATTACCTGACCATTCTGATTGGGGCTTTGTGGTCTGCTGGGCCCCCTTCT
|||||
AGGAGCGATTACCTTGACCATCCTGATTGGCGTCTTTGTTGTCTGCTGGGCCCCATTCT
1120 1130 1140 1150 1160 1170

con-mc4r.seq 580 590 600 610 620 630
TCCTCCACTTAATAATTCTATATCTCCTGCCCCAGAAATCCATACTGTGTGTCTTCATGT
|||||
TCCTCCACTTAATAATTCTACATCTCTGTCCCTCAGAATCCATATTGTGTGTCTTCATGT
1180 1190 1200 1210 1220 1230

con-mc4r.seq 640 650 660 670 680 690
CTCAGTTTAAATTGTATCTCATCTCTGATCATGTGTAAATCCATCATCAATCCCCTGATTT
|||||
CTCAGTTTAACTTGTATCTCATCTCTGATCATGTGTAAATCCATCATCAATCCCCTGATTT
1240 1250 1260 1270 1280 1290

con-mc4r.seq 700 710 720 730 740
ATGCACTCCGGAGCCCAAGAACTGAGGAAACCTTCAAAGAGATCATCTGTGTCTAT
|||||
ATGCACTCCGGAGTCAAGAACTGAGGAAACCTTCAAAGAGATCATCTGTGTCTATCCCC
1300 1310 1320 1330 1340 1350

s77415 TGGGAGGCCCTTTGTGACTTGTCTAGCAGATATTAAATGGGGACAGACGCAATATAGG
1360 1370 1380 1390 1400 1410
```

Fig. 2C

human.pcp
mc4r-allele

	110	120	130	140	150	160
human.pcp	IITLLNSTDTDAQSFTVNIDNVIDSVICSSLLASICSLLSIAVDRYFTTFYALQYHNIMT					
	:					
mc4r-allele	VITLLNSTDTDAQSFTVNIDNVIDSVICSSLLASICSLLSIAVDRYFTTFYALQYHNIMT					

	170	180	190	200	210	220
human.pcp	VKRVGISISCIWAAC	TVSGILFI	YSDSSAVI	CLITMFF	TALMASLY	VHMFMLMARLH
mc4r-allele	VKRVGIIISCIWAVC	TVSGVLFI	YSDSSAVI	CLITVFF	TALMASLY	VHMFMLMARLH
	100	110	120	130	140	150

[illegible]

	290	300	310	320	330
human.pcp	HFNLVLLIMCNSIIDPLIYALRSQELRKT	FKEIICCYPLGG	CDLSSRY		
mc4r-allele	HFNLVLLIMCNSIIDPLIYALRSQELRKT	FKEIICCY			
	220	230	240		

Fig. 3A

Fig. 3B

8/13

S0082	MC4R	rec. frags.=	0.05,	lods =	14.74
CGA	MC4R	rec. frags.=	0.14,	lods =	6.88
S0020	MC4R	rec. frags.=	0.18,	lods =	5.32
S0079	MC4R	rec. frags.=	0.12,	lods =	10.35
S0155	MC4R	rec. frags.=	0.14,	lods =	7.68
S0122	MC4R	rec. frags.=	0.18,	lods =	5.17
S0313	MC4R	rec. frags.=	0.00,	lods =	17.76
S0312	MC4R	rec. frags.=	0.20,	lods =	5.60
S0311	MC4R	rec. frags.=	0.17,	lods =	7.18
S0416	MC4R	rec. frags.=	0.20,	lods =	3.21
S0331	MC4R	rec. frags.=	0.02,	lods =	21.91
S0396	MC4R	rec. frags.=	0.16,	lods =	7.85
BHT0433	MC4R	rec. frags.=	0.02,	lods =	21.32
S0536	MC4R	rec. frags.=	0.03,	lods =	15.61
CAPN3	MC4R	rec. frags.=	0.12,	lods =	6.65

Fig. 4A

9/13

KGF	MC4R	rec. frags.=	0.09,	lods =	6.46
MEF2A	MC4R	rec. frags.=	0.05,	lods =	14.36
MC4R	MC4R	rec. frags.=	0.00,	lods =	26.19
S0082	MC4R	rec. frags.=	0.00	0.09,	lods = 15.86
CGA	MC4R	rec. frags.=	0.07	0.22,	lods = 7.46
S0020	MC4R	rec. frags.=	0.00	0.25,	lods = 6.33
S0079	MC4R	rec. frags.=	0.00	0.19,	lods = 11.48
S0155	MC4R	rec. frags.=	0.00	0.24,	lods = 9.98
S0122	MC4R	rec. frags.=	0.00	0.27,	lods = 7.10
S0313	MC4R	rec. frags.=	0.00	0.00,	lods = 17.76
S0312	MC4R	rec. frags.=	0.04	0.29,	lods = 7.45

Fig. 4B

10/13

S0311	MC4R	rec.	fracs.=	0.00	0.28,	lods =	9.02
S0416	MC4R	rec.	fracs.=	0.00	0.31,	lods =	4.17
S0331	MC4R	rec.	fracs.=	0.05	0.00,	lods =	22.14
S0396	MC4R	rec.	fracs.=	0.03	0.24,	lods =	9.33
BHT0385	MC4R	rec.	fracs.=	0.14	0.36,	lods =	3.46
BHT0433	MC4R	rec.	fracs.=	0.05	0.00,	lods =	21.82
S0536	MC4R	rec.	fracs.=	0.00	0.05,	lods =	15.77
CAPN3	MC4R	rec.	fracs.=	0.00	0.18,	lods =	7.35
KGF	MC4R	rec.	fracs.=	0.00	0.17,	lods =	6.74
MEF2A	MC4R	rec.	fracs.=	0.10	0.00,	lods =	14.52
MC4R	MC4R	rec.	fracs.=	0.00	0.00,	lods =	26.19

Fig. 4C

11/13

0	ESR		0.0
		0.18	18.4
1	S0008		18.4
		0.12	11.9
7	CGA		30.3
		0.03	2.8
3	S0312		33.1
		0.05	4.9
4	S0122		38.1
		0.09	9.4
8	KGF		47.4
		0.06	5.8
6	CAPN3		53.2
		0.02	2.5
9	MEF2A		55.7
		0.06	6.1
5	MC4R		61.8
		0.06	5.6
10	S0313		67.4
		0.00	0.0
11	S0082		67.4
		0.03	3.4
12	S0079		70.8
		0.03	2.5
14	S0142		73.3
		0.01	1.0
13	S0020		74.4
		0.04	4.3
15	S0311		78.7
		0.00	0.0
16	S0155		78.7
		0.12	12.2
17	S0113		90.9
		0.20	21.0
18	S0302		111.9
		0.22	23.4
19	S0112		135.3

Fig. 4D

12/13



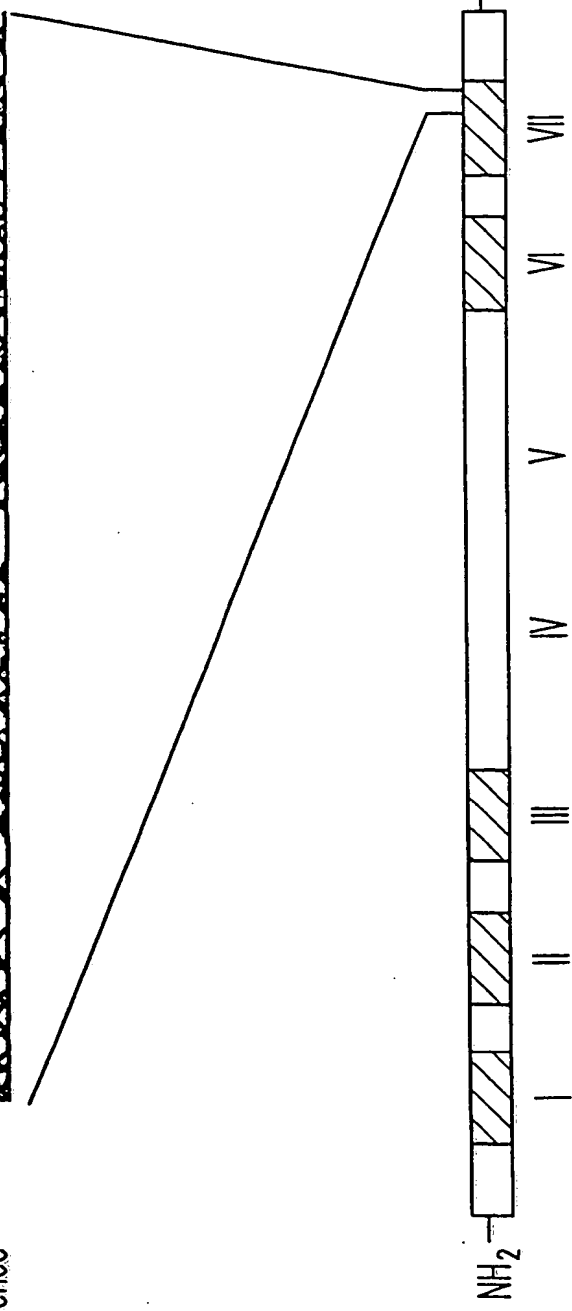
Allele 1
homozygote
sequence

293 C N S L I D P L I Y
295 S L I D P L I Y
297
299
300

GTGTAATTCCATCATCGATCCCTGATTTATGCG

Allele 2
homozygote
sequence

C N S L I D P L I Y
GTGTAATTCCATCATCGATCCCTGATTTATGCG





 = Transmembrane domains

Fig. 5

13/13



pMC4RMSHFNLYLILIMCNSIIDPLIYAL.....*
hMC4RMSHFNLYLILIMCNSIIDPLIYAL..... 304
rMC4RMSHFNLYLILIMCNAVIDPLIYAL..... 304
sheep MC5RMSHFNMYLILIMCNSVIDPLIYA..... 286
bovine MC5RMSHFNMYLILIMCNSVIDPLIYA..... 286
bovine MC2RMSLFQVNGVLIMCNAIIDPFIYAL..... 268
hMC3RAHFNTYLVLIMCNSVIDPLIYA..... 327
mMC3RAHFNTYLVLIMCNSVIDPLIYA..... 290
hMC2RMSHFNMYLILIMCNSVMDPLIYA..... 268
hMC1RSYFNLFLLILIIICNSVVDPLIYA..... 299
bEDG-2RLAYEKFFLLLAEFNSAMNP I IYSYR.... 314
hEDG-4RFLLLAEANSLVNAAVYSCR.... 298
human cannabVFAFCSMLCLLNSTVNPLIYAL..... 399
hH2ABFQFFFWIGYCNSSLNPVIYTI..... 290
rSSR2FDFVVILT YANSCANP ILYAFL.... 315
hGAL1-RLAYSNSSVNP I IYAF L.... 306

Fig. 6